

Sequences producing significant alignments:

Score E
(bits) Value

gi 9755159 gb AAF98175.1 AF285167_1	ATP-binding cassette tr...	589	e-167	■
gi 13876613 gb AAK43526.1 AF287262_1	ATP-binding cassette 1...	589	e-167	■
gi 21536376 ref NP_005493.2	ATP-binding cassette, sub-fami...	588	e-167	■
gi 9247086 gb AAF86276.1 AF275948_1	ABCA1 [Homo sapiens]	585	e-166	■
gi 5734135 gb AAD49852.1	ATP cassette binding transporter ...	585	e-166	■
gi 4128033 emb CAA10005.1	ATP-binding cassette transporter...	585	e-166	■
gi 13123945 sp O95477 ABC1_HUMAN	ATP-binding cassette, sub-...	585	e-166	■
gi 7304849 ref NP_038482.1	ATP-binding cassette 1, sub-fam...	549	e-155	■
gi 13124694 sp P41233 ABC1_MOUSE	ATP-binding cassette, sub-...	549	e-155	■
gi 11611825 gb AAG39073.1 AF287263_1	ATP-binding cassette 1...	541	e-153	■
gi 27714435 ref XP_232954.1	similar to ABCA1 [Homo sapiens]...	498	e-140	■
gi 18028983 gb AAL56247.1 AF362377_1	ATP-binding cassette t...	472	e-132	■
gi 27806343 ref NP_776646.1	ATP-binding cassette, sub-fami...	288	4e-77	■
gi 2959643 gb AAC05632.1	rim ABC transporter [Homo sapiens]	287	9e-77	■
gi 2969966 emb CAA75729.1	ABCR [Homo sapiens]	287	1e-76	■
gi 6707663 sp P78363 ABCR_HUMAN	Retinal-specific ATP-bindin...	287	1e-76	■
gi 4557876 ref NP_000341.1	ATP-binding cassette, sub-famil...	287	1e-76	■
gi 3243082 gb AAC23915.1	ATP-binding cassette transporter ...	287	1e-76	■
gi 6671495 ref NP_031404.1	ATP-binding cassette, sub-famil...	286	3e-76	■
gi 12656651 gb AAK00959.1 AF328787_1	ABC transporter member...	244	1e-63	■
gi 15451838 ref NP_150651.1	ATP-binding cassette, sub-fami...	243	3e-63	■

gi 9506365 ref NP_061985.1	ATP-binding cassette, sub-famil...	242	5e-63	
gi 22725156 gb AA04657.1	ABC transporter ABCA7 [Homo sapi...	241	8e-63	
gi 15451840 ref NP_038878.1	ATP-binding cassette, sub-fami...	239	3e-62	
gi 26342298 dbj BAC34811.1	unnamed protein product [Mus mu...	228	7e-59	
gi 20521748 dbj BAA83014.2	KIAA1062 protein [Homo sapiens]	100	4e-20	
gi 11346269 pir A59189	ATP-binding cassette transporter - ...	98	1e-19	
gi 14916523 sp Q9BZC7 ABC2_HUMAN	ATP-binding cassette, sub-...	98	1e-19	
gi 14550412 ref NP_001597.1	ATP-binding cassette, sub-fami...	98	1e-19	
gi 11993939 ref NP_031405.1	ATP-binding cassette, sub-fami...	97	2e-19	
gi 14250599 gb AAH08755.1 AAH08755	Similar to KIAA1062 prot...	97	3e-19	
gi 1082239 pir B54774	ATP binding cassette transporter ABC...	96	7e-19	
gi 13242308 ref NP_077372.1	ATP-binding cassette, sub-fami...	95	1e-18	
gi 27881503 ref NP_775099.1	ATP-binding cassette, sub-fami...	82	1e-14	
gi 27881501 ref NP_056472.2	ATP-binding cassette, sub-fami...	82	1e-14	
gi 23957299 gb AA040735.1 AF418105_1	ATP-binding cassette t...	82	1e-14	
gi 14189735 gb AAK54355.1	ATP-binding cassette transporter...	82	1e-14	
gi 27684549 ref XP_237242.1	similar to ATP-binding cassett...	75	1e-12	
gi 25141343 ref NP_490949.2	ABC transporter family member ...	72	1e-11	
gi 7498949 pir T15200	hypothetical protein F12B6.1 - Caeno...	71	2e-11	
gi 21297828 gb EAA09973.1	agCP11808 [Anopheles gambiae str...	59	1e-07	
gi 20850354 ref XP_136692.1	similar to ATP-binding cassett...	58	1e-07	
gi 24643648 ref NP_608437.1	CG1819-PA [Drosophila melanoga...	47	3e-04	
gi 27697650 ref XP_223630.1	similar to hypothetical protei...	39	0.11	
gi 15610478 ref NP_217859.1	hypothetical protein Rv3342 [M...	34	2.3	
gi 15842938 ref NP_337975.1	methyltransferase, putative [M...	34	2.4	
gi 20088939 ref NP_615014.1	conserved hypothetical protein...	34	2.6	
gi 1172578 sp Q08304 PPOB_LYCES	Polyphenol oxidase B, chlor...	34	2.8	
gi 20899064 ref XP_139895.1	similar to ATP-binding cassett...	33	3.2	
gi 21227448 ref NP_633370.1	Fe-S oxidoreductase [Methanosa...	33	4.3	
gi 27378790 ref NP_770319.1	blr3679 [Bradyrhizobium japoni...	33	5.1	

Alignments

Get selected sequences

Select all

Deselect all

☒ >gi|9755159|gb|AAF98175.1|AF285167_1 ATP-binding cassette transporter 1 [Homo
Length = 2261

Score = 589 bits (1519), Expect = e-167
Identities = 283/284 (99%), Positives = 283/284 (99%)

Query: 1 FGKYPSELELPWYNYTFVSNAPEDTGTELLNALT KDPGFGTRCMEGNPIPDTPCQ 60
FGKYPSELELPWYNE YTFVSNAPEDTGTELLNALT KDPGFGTRCMEGNPIPDTPCQ
Sbjct: 1371 FGKYPSELELPWYNEQYTFVSNAPEDTGTELLNALT KDPGFGTRCMEGNPIPDTPCQ 1430


Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK
Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSQE 180

QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE
 Sbjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1550

Query: 181 VNDIAIKQMKKHLKLAkdSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDIAIKQMKKHLKLAkdSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 1551 VNDIAIKQMKKHLKLAkdSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTkQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTkQQLSEVALMTTSVD
 Sbjct: 1611 NAILRANLQKGENPSHYGITAFNHPLNLTkQQLSEVALMTTSVD 1654

 >gi|13876613|gb|AAK43526.1|AF287262_1 ATP-binding cassette 1 sub-family A member
 Length = 2261

Score = 589 bits (1519), Expect = e-167
 Identities = 283/284 (99%), Positives = 283/284 (99%)



Query: 1 FGKYPSELELQPWMYNENYTFVSNDAPEdTGtLELLNALTkdPGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELELQPWMYNE YTFVSNDAPEdTGtLELLNALTkdPGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELELQPWMYNEQYTFVSNDAPEdTGtLELLNALTkdPGFGTRCMEGNPIPDTPCQ 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE
 Sbjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1550

Query: 181 VNDIAIKQMKKHLKLAkdSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDIAIKQMKKHLKLAkdSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 1551 VNDIAIKQMKKHLKLAkdSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTkQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTkQQLSEVALMTTSVD
 Sbjct: 1611 NAILRANLQKGENPSHYGITAFNHPLNLTkQQLSEVALMTTSVD 1654

 >gi|21536376|ref|NP_005493.2|  ATP-binding cassette, sub-family A member 1; AT
 high density lipoprotein deficiency, Tangier type, 1;
 cholesterol efflux regulatory protein [Homo sapiens]
 gi|15212107|dbj|BAB63210.1| ABCA1 [Homo sapiens]
 Length = 2261

Score = 588 bits (1515), Expect = e-167
 Identities = 282/284 (99%), Positives = 283/284 (99%)

Query: 1 FGKYPSELELQPWMYNENYTFVSNDAPEdTGtLELLNALTkdPGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELELQPWMYNE YTFVSNDAPEdTGtLELLNALTkdPGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELELQPWMYNEQYTFVSNDAPEdTGtLELLNALTkdPGFGTRCMEGNPIPDTPCQ 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180

QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE
Sbjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1550

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLD+NNVKVWFNNKGWHAISSFLNVIN
Sbjct: 1551 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTKNNVKVWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
Sbjct: 1611 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

>gi|9247086|gb|AAF86276.1|AF275948.1 ABCA1 [Homo sapiens]
Length = 2261

Score = 585 bits (1509), Expect = e-166
Identities = 281/284 (98%), Positives = 281/284 (98%)

Query: 1 FGKYPSELELQPWMYNENYTFVSNDAPEdTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
FGKYPSELELQPWMYNE YTFVSNDAPEdTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ
Sbjct: 1371 FGKYPSELELQPWMYNEQYTFVSNDAPEdTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK
Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE
Sbjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1550

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
VNDA KQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN
Sbjct: 1551 VNDAXKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVA MTTSVD
Sbjct: 1611 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAXMTTSVD 1654

>gi|5734135|gb|AAD49852.1| ATP cassette binding transporter 1 [Homo sapiens]
Length = 849

Score = 585 bits (1507), Expect = e-166
Identities = 282/284 (99%), Positives = 283/284 (99%)

Query: 1 FGKYPSELELQPWMYNENYTFVSNDAPEdTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
FGKYPSELELQPWMYNE YTFVSNDAPEdTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ
Sbjct: 428 FGKYPSELELQPWMYNEQYTFVSNDAPEdTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 487

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK
Sbjct: 488 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 547

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE
Sbjct: 548 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 607

Query: 181 VNDAIKQMKKHLKLAkdSSADrFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDAIKQMKKHLKLAkdSSADrFLNSLGRFMTGLDT+NNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 608 VNDAIKQMKKHLKLAkdSSADrFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 667

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 668 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 711

☐ >gi|4128033|emb|CAA10005.1| ☒ ATP-binding cassette transporter-1 (ABC-1) [Homo s
 gi|5734101|gb|AAD49849.1|AF165281_1 ☒ ATP cassette binding transporter 1 [Homo sa
 Length = 2201

Score = 585 bits (1507), Expect = e-166
 Identities = 281/284 (98%), Positives = 281/284 (98%)

Query: 1 FGKYPSELELPWMYNENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELELPWMYNE YTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ
 Sbjct: 1311 FGKYPSELELPWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 1370

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1371 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1430

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE
 Sbjct: 1431 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1490

Query: 181 VNDAIKQMKKHLKLAkdSSADrFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDA KQMKKHLKLAkdSSADrFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 1491 VNDATKQMKKHLKLAkdSSADrFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 1550

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVA MTTSVD
 Sbjct: 1551 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVD 1594

☐ >gi|13123945|sp|O95477|ABC1_HUMAN ATP-binding cassette, sub-family A, member 1
 transporter 1) (ATP-binding cassette 1) (ABC-1)
 (Cholesterol efflux regulatory protein)
 Length = 2261

Score = 585 bits (1507), Expect = e-166
 Identities = 281/284 (98%), Positives = 281/284 (98%)

Query: 1 FGKYPSELELPWMYNENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELELPWMYNE YTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELELPWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE
 Sbjct: 1491 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 1550

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDA KQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 1551 VNDATKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVA MTTSVD
 Sbjct: 1611 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVD 1654

>gi|7304849|ref|NP_038482.1| ATP-binding cassette 1, sub-family A, member 1; 1
 1 [Mus musculus]
 gi|1082238|pir||A54774 ATP binding cassette transporter ABC1 - mouse
 gi|495257|emb|CAA53530.1| ABC transporter [Mus musculus]
 Length = 2201

Score = 549 bits (1414), Expect = e-155
 Identities = 263/284 (92%), Positives = 273/284 (96%)

Query: 1 FGKYPSELELQPMYENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELELQPMYNE YTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPC
 Sbjct: 1311 FGKYPSELELQPMYNEQYTFVSNDAPEDMGTQELLLNALTKDPGFGTRCMEGNPIPDTPCL 1370

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEE+WT +PVPQ+I+DLFQNGNWTM+NPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1371 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1430

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
 Q TADILQ+LTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPS E
 Sbjct: 1431 QKTADILQNLTLGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNSQALPPSHE 1490

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDAIKQMKK LKL KD+SADRFL+SLGRFM GLDT+NNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 1491 VNDAIKQMKKLLKLT KDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVIN 1550

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1551 NAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1594

>gi|13124694|sp|P41233|ABC1_MOUSE ATP-binding cassette, sub-family A, member 1
 transporter 1) (ATP-binding cassette 1) (ABC-1)
 Length = 2261

Score = 549 bits (1414), Expect = e-155
 Identities = 263/284 (92%), Positives = 273/284 (96%)

Query: 1 FGKYPSELELQPMYENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELELQPMYNE YTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPC
 Sbjct: 1371 FGKYPSELELQPMYNEQYTFVSNDAPEDMGTQELLLNALTKDPGFGTRCMEGNPIPDTPCL 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEE+WT +PVPQ+I+DLFQNGNWTM+NPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1431 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
 Q TADILQ+LTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPS E
 Sbjct: 1491 QKTADILQNLTLGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNSQALPPSHE 1550

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDAIKQMKK LKL KD+SADRFL+SLGRFM GLDT+NNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 1551 VNDAIKQMKKLLKLT KDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1611 NAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

 >gi|11611825|gb|AAG39073.1|AF287263_1  ATP-binding cassette 1, sub-family A, me
 Length = 2198

Score = 541 bits (1394), Expect = e-153
 Identities = 262/284 (92%), Positives = 271/284 (95%), Gaps = 2/284 (0%)



Query: 1 FGKYPSELELQPWMYNENYTFVSNDAPE DTGTLELLNALT KD PGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELELQPWMYNE YTFVSNDAPE DT GT ELLNALT KD PGFGTRCMEGNPIPDTPC
 Sbjct: 1311 FGKYPSELELQPWMYNEQYTFVSNDAPE DMGTQELLNALT KD PGFGTRCMEGNPIPDTPC 1370

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGE+WT +PVPQ+I+DLFQNGNWTM+NPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1371 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1430

Query: 121 QNTADILQDLTGRNISDYL VKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
 Q TADILQ+LTGRNISDYL VKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPS E
 Sbjct: 1431 QKTADILQNL TGRNISDYL VKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSHE 1490

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDAIKQMKK LKL K SADRFL+SLGRFM GLDT+NNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 1491 VNDAIKQMKKLLKLT K--SADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVIN 1548

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1549 NAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1592

 >gi|27714435|ref|XP_232954.1|  similar to ABCA1 [Homo sapiens] [Rattus norvegicus]
 Length = 978

Score = 498 bits (1283), Expect = e-140
 Identities = 239/262 (91%), Positives = 252/262 (96%)

Query: 1 FGKYPSELELQPWMYNENYTFVSNDAPE DTGTLELLNALT KD PGFGTRCMEGNPIPDTPCQ 60
 FGKYP+LELQPWMYNE YTFVSNDAPE DT GT ELLNALT KD PGFGTRCMEGNPIP+TPC
 Sbjct: 61 FGKYPNLELQPWMYNEQYTFVSNDAPE DMGTQELLNALT KD PGFGTRCMEGNPIPNTPC 120

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 GEE+WTT PVPQT+MDLFQNGNWTM+NPSP+QCSSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 121 VGEEDWTTGPVPQTLMDLFQNGNWTMKNPSPSCQCSSDKIKKMLPVCPPGAGGLPPPQRK 180

Query: 121 QNTADILQDLTGRNISDYL VKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
 Q TADILQ+LTGRNISDYL VKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE
 Sbjct: 181 QKTADILQNL TGRNISDYL VKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 240


Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VN+AIKQMKK LKL KDSSADRFL+SLGRFMTGLDT+NNVKVWFNNKGWHAISSFLNVIN

Sbjct: 241 VNNAIKQMKKLLKLTkdssadrflsslgrfMTGLDtknnvkVWFNnkgWHAISSFLNVIN 300

Query: 241 NAILRANLQKGENPSHYGITAF 262

NAILRANLQKGENPS YGITAF

Sbjct: 301 NAILRANLQKGENPSQYGITAF 322

 >gi|18028983|gb|AAL56247.1|AF362377.1 ATP-binding cassette transporter 1 [Gallus
Length = 2260

Score = 472 bits (1215), Expect = e-132

Identities = 223/284 (78%), Positives = 256/284 (90%), Gaps = 1/284 (0%)

Query: 1 FGKYPSELELQPMYENYTFVSNDAPEdTGtLEllNALTKDPGFGTRCMegNPIPDTPCQ 60

FGKYPSELELQPMY+E YTF+SNDAPED GT +LL+AL PGFGTRCM+G+ IPDTPC

Sbjct: 1371 FGKYPSELELQPMYDEQYTFISNDAPEDAGTQKLlDALLNKPGFGTRCMQGHsIPDTPCT 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSpacQcSSDKIKKMLPVCPPGAGGLPPPQRK 120

G++EWTTA VP +++++ + GNW+M+NPS+P+C+CS++KIKKMLPVCPPGAGGLPPPQR+

Sbjct: 1431 VGQKEWTTASVPDSVLEILR-GNWSMENPSPSCECSNEKIKKMLPVCPPGAGGLPPPQRE 1489

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180

Q+TADILQ+LTGRNISDYLVKTY QII KSLKNKIWVNEFRYGGFSLG ++ LPPS E

Sbjct: 1490 QDTADILQNLtGRNISDYLVKTYAQIIGKSLKNKIWVNEFRYGGFSLGARSShVLPpSNE 1549

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNnkgWHAISSFLNVIN 240




V DAIKQ+KK L+LA+ SS DRFLN+L FM GLDT+NNVKVWFNnkgWHAi+SFLNVIN

Sbjct: 1550 VTDAIKQVKKILELAQGSsGDRFLNNLASFMKGLDtknnvkVWFNnkgWHAIASFLNVIN 1609

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284

NAILRANLQ+G+NPS YGITAFNHPLNLTKQQLSEVALMTTSVD

Sbjct: 1610 NAILRANLQQGKNPSAYGITAFNHPLNLTKQQLSEVALMTTSVD 1653

 >gi|27806343|ref|NP_776646.1|  ATP-binding cassette, sub-family A (ABC1), member
gi|1943947|gb|AAC48716.1|  ABC transporter [Bos taurus]
Length = 2281

Score = 288 bits (738), Expect = 4e-77

Identities = 137/286 (47%), Positives = 180/286 (62%), Gaps = 5/286 (1%)

Query: 1 FGKYPSELELQPMYENYTFVSNDAPEdTGtLEllNALTKDPGFGTRCMegNPIPDTPCQ 60

FG+YP+L L PWMY + YTF S D P+ L + L PGFG RC++ +P+ PC

Sbjct: 1395 FGEYPALTLHPWMYGGQYTFfSMDQPDSEWLSALADVLVNKPGFGNRCLKEEWLPEFPC- 1453

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMqNPSpacQcSSDKIKKMLPVCPPGAGGLPPPQRK 120

W T V + L Q WT PSP+C+CS+ + MLP CP GAGGLPPPQR

Sbjct: 1454 GNSSPWKTPSVSPDVTHLLQQQKWTADQPSpSCRCSTREKLTMLPECPEGAGGLPPPQRI 1513

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPP--S 178

Q + +ILQDLT RN+SD+LVKTY +I SLK+K WVNE RYGG S+G PP

Sbjct: 1514 QRSTEILQDLTDRNVSDFLVKTYPALIRSSLKSKFWVNEQRYGGISVG--GKLPApPFTG 1571

Query: 179 QEVDNAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNnkgWHAISSFLNV 238

+ + + + + + + F+ L+T +N+KVWFNnkgWHA+ SFLNV

Sbjct: 1572 EALVGFLSDLGQLMNVSGGPMTREAAKEMPAFLKQLETEdNIKVWFNnkgWHAIVSFLNV 1631

Query: 239 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NAILRA+L K +NP YGIT + PLNLTK+QLSE+ ++TTSVD
 Sbjct: 1632 AHNAILRASLHKDKNPPEYGITVISQPLNLTKQLSEITVLTTTSVD 1677

>gi|2959643|gb|AAC05632.1| rim ABC transporter [Homo sapiens]
 Length = 2273

Score = 287 bits (735), Expect = 9e-77
 Identities = 140/285 (49%), Positives = 181/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELELQPMYNNENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
 FG+YP+L L PW+Y + YTF S D P L + L PGFG RC++ +P+ PC
 Sbjct: 1397 FGEYPALTLHPWIYQQYTFFSMDEPGSEQFTVLADVLLNKPFGNRCLEKGLPEYPC- 1455

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 W T V I LFQ WT NPSP+C+CS+ + MLP CP GAGGLPPPQR
 Sbjct: 1456 GNSTPWKTPCVSPNITQLFQKQKWTQVNPSPSCRCSTREKLTMLPECPEGAGGLPPPQRT 1515

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
 Q T +ILQDLT RNISD+LVKTY +I SLK+K WVNE RYGG S+G +P + E
 Sbjct: 1516 QRTTEILQDLTDRNISDFLVKTYPALIRSSLKSKFWVNEQRYGGISIG-GKLPVVPITGE 1574

Query: 181 -VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
 + + + + + + F+ L+T +N+KVWFNNKGWHA+ SFLNV
 Sbjct: 1575 ALVGFLSDLGRIMNVSGGPITREASKEIPDFLKHLETEDNIKVWFNNKGWHALVSFLNVA 1634

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NAILRA+L K +P YGIT + PLNLTK+QLSE+ ++TTSVD
 Sbjct: 1635 HNAILRASLPKDRSPPEYGITVISQPLNLTKQLSEITVLTTTSVD 1679

>gi|2969966|emb|CAA75729.1| ABCR [Homo sapiens]
 Length = 2273

Score = 287 bits (735), Expect = 1e-76
 Identities = 139/285 (48%), Positives = 181/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELELQPMYNNENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
 FG+YP+L L PW+Y + YTF S D P L + L PGFG RC++ +P+ PC
 Sbjct: 1397 FGEYPALTLHPWIYQQYTFFSMDEPGSEQFTVLADVLLNKPFGNRCLEKGLPEYPC- 1455

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 W T V I LFQ WT NPSP+C+CS+ + MLP CP GAGGLPPPQR
 Sbjct: 1456 GNSTPWKTPSVSPNITQLFQKQKWTQVNPSPSCRCSTREKLTMLPECPEGAGGLPPPQRT 1515

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
 Q + +ILQDLT RNISD+LVKTY +I SLK+K WVNE RYGG S+G +P + E
 Sbjct: 1516 QRSTEILQDLTDRNISDFLVKTYPALIRSSLKSKFWVNEQRYGGISIG-GKLPVVPITGE 1574

Query: 181 -VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
 + + + + + + F+ L+T +N+KVWFNNKGWHA+ SFLNV
 Sbjct: 1575 ALVGFLSDLGRIMNVSGGPITREASKEIPDFLKHLETEDNIKVWFNNKGWHALVSFLNVA 1634

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NAILRA+L K +P YGIT + PLNLTK+QLSE+ ++TTSVD
 Sbjct: 1635 HNAILRASLPKDRSPPEYGITVISQPLNLTKQLSEITVLTTTSVD 1679

>gi|6707663|sp|P78363|ABCR_HUMAN Retinal-specific ATP-binding cassette transport transporter) (RIM protein) (RMP) (Stargardt disease protein)
Length = 2273

Score = 287 bits (734), Expect = 1e-76

Identities = 139/285 (48%), Positives = 181/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELELPWMYENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
FG+YP+L L PW+Y + YTF S D P L + L PGFG RC++ +P+ PC
Sbjct: 1397 FGEYPALTLHPWIYQQYTFFSMDEPGSEQFTVLADVLLNKPFGNRCLEKGLPEYPC- 1455

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
W T V I LFQ WT NPSP+C+CS+ + MLP CP GAGGLPPPQR
Sbjct: 1456 GNSTPWKTPSVSPNITQLFQKQKWTQVNPSPSCRCSTREKLTMLPECPEGAGGLPPPQRT 1515

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
Q + +ILQDLT RNISD+LVKTY +I SLK+K WVNE RYGG S+G +P + E
Sbjct: 1516 QRSTEILQDLTDRNISDFLVKTYPALIRSSSLKSKFWVNEQRYGGISIG-GKLPVVPITGE 1574

Query: 181 -VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
+ + + + + + + F+ L+T +N+KVWFNNKGWHA+ SFLNV
Sbjct: 1575 ALVGFLSDLGRIMNVSGGPITREASKEIPDFLKHLETEDNIKVWFNNKGWHALVSFLNVA 1634

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQLSEVALMTTSVD 284
+NAILRA+L K +P YGIT + PLNLTK+QLSE+ ++TTSVD
Sbjct: 1635 HNAILRASLPKDRSPEEYGITVISQPLNLTKQLSEITVLTTSVD 1679

>gi|4557876|ref|NP_000341.1| ATP-binding cassette, sub-family A member 4; ATP transporter; ATP-binding transporter, retina-specific; rim protein [Homo sapiens]
gi|1888527|gb|AAC51144.1| ATP-binding cassette transporter [Homo sapiens]
Length = 2273

Score = 287 bits (734), Expect = 1e-76

Identities = 139/285 (48%), Positives = 181/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELELPWMYENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
FG+YP+L L PW+Y + YTF S D P L + L PGFG RC++ +P+ PC
Sbjct: 1397 FGEYPALTLHPWIYQQYTFFSMDEPGSEQFTVLADVLLNKPFGNRCLEKGLPEYPC- 1455

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
W T V I LFQ WT NPSP+C+CS+ + MLP CP GAGGLPPPQR
Sbjct: 1456 GNSTPWKTPSVSPNITQLFQKQKWTQVNPSPSCRCSTREKLTMLPECPEGAGGLPPPQRT 1515

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
Q + +ILQDLT RNISD+LVKTY +I SLK+K WVNE RYGG S+G +P + E
Sbjct: 1516 QRSTEILQDLTDRNISDFLVKTYPALIRSSSLKSKFWVNEQRYGGISIG-GKLPVVPITGE 1574

Query: 181 -VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
+ + + + + + + F+ L+T +N+KVWFNNKGWHA+ SFLNV
Sbjct: 1575 ALVGFLSDLGRIMNVSGGPITREASKEIPDFLKHLETEDNIKVWFNNKGWHALVSFLNVA 1634

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQLSEVALMTTSVD 284

+NAILRA+L K +P YGIT + PLNLTK+QLSE+ ++TTSVD
 Sbjct: 1635 HNAILRASLPKDRSPEEYGITVISQPLNLTKQLSEITVLTTSD 1679

☐ >gi|3243082|gb|AAC23915.1| ☒ ATP-binding cassette transporter [Homo sapiens]
 Length = 2273

Score = 287 bits (734), Expect = 1e-76
 Identities = 139/285 (48%), Positives = 181/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELELQPMYNNENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMENPIPDTPCQ 60
 FG+YP+L L PW+Y + YTF S D P L + L PGFG RC++ +P+ PC
 Sbjct: 1397 FGEYPALTLHPWIYQQYTFFSMDEPGSEQFTVLADVLLNKPFGFNRCLKEGWLPEYPC- 1455

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 W T V I LFQ WT NPSP+C+CS+ + MLP CP GAGGLPPPQR
 Sbjct: 1456 GNSTPWKTPSVSPNITQLFQKQKWTQVNPSPSCRCSTREKLTMLPECPEGAGGLPPPQRT 1515

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
 Q + +ILQDLT RNISD+LVKTY +I SLK+K WVNE RYGG S+G +P + E
 Sbjct: 1516 QRSTEILQDLTDRNISDFLVKTYPALIRSSLSKSKFWVNEQRYGGISIG-GKLPVVPITGE 1574

Query: 181 -VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
 + + + + + + F+ L+T +N+KVWFNNKGWHA+ SFLNV
 Sbjct: 1575 ALVGFLSDLGRIMNVSGGPITREASKEIPDFLKHLETEDNIKVWFNNKGWHALVSFLNVA 1634

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSD 284
 +NAILRA+L K +P YGIT + PLNLTK+QLSE+ ++TTSVD
 Sbjct: 1635 HNAILRASLPKDRSPEEYGITVISQPLNLTKQLSEITVLTTSD 1679

☐ >gi|6671495|ref|NP_031404.1| ☒ ATP-binding cassette, sub-family A, member 4; ATI
 10; Rim protein [Mus musculus]

gi|2547314|gb|AAC23916.1| ☒ ATP-binding cassette transporter [Mus musculus]
 Length = 2310

Score = 286 bits (731), Expect = 3e-76
 Identities = 138/285 (48%), Positives = 182/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELELQPMYNNENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMENPIPDTPCQ 60
 FG++P+L L PAMY YTF S D P + L + L PGFG RC++ +P+ PC
 Sbjct: 1396 FGEFPALTLHPWYGHQYTFFSMDEPNNEHLEVLADVLLNRPFGFNRCLKEEWLPEYPC- 1454

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 W T V I LFQ WT +PSP+C+CS+ + MLP CP GAGGLPPPQR
 Sbjct: 1455 INATSWKTPSVSPNITHLFQKQKWTAAHPSPSCKCSTREKLTMLPECPEGAGGLPPPQRT 1514

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
 Q + ++LQDLT RNISDYLVKTY +I SLK+K WVNE RYGG S+G A+P S E
 Sbjct: 1515 QRSTEVLQDLTNRNISDYLVKTYPALIRSSLSKSKFWVNEQRYGGISIG-GKLPAPISGE 1573

Query: 181 -VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
 + + + + + + F+ L+T +N+KVWFNNKGWHA+ SFLNV
 Sbjct: 1574 ALVGFLSGLGQMMNVSGGPVTREASKEMLDFLKHLETTDNIKVWFNNKGWHALVSFLNVA 1633

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSD 284
 +NAILRA+L + +P YGIT + PLNLTK+QLS++ ++TTSVD

Sbjct: 1634 HNAILRASLPRDRDPEEYGITVISQPLNLTKEQLSDITVLTTSD 1678

☐ >gi|12656651|gb|AAK00959.1|AF328787.1 ☒ ABC transporter member 7 [Homo sapiens]
Length = 2146

Score = 244 bits (622), Expect = 1e-63

Identities = 126/284 (44%), Positives = 176/284 (61%), Gaps = 11/284 (3%)

Query: 1 FGKYPSELELQPMYNNENYTFVSNDAPEDTGTLELLNALT KDPGFGTRCMEGNPIPDTPCQ 60
FG YP+L L P MY +F S DAP D G LL AL ++ G + + P Q
Sbjct: 1263 FGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARLLEALLQEAG-----LEEPPVQ 1312

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
++ VP + + +GNWT ++PSPACQCS +++LP CP AGG PPPQ
Sbjct: 1313 HSSHRFSAPEVPAEVAKVLASGNWTPESPSPACQCSRPGARRLLPDCPAAAGGPPPPQAV 1372

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
+ +++Q+LTGRN+SD+LVKTY +++ + LK K WVNE RYGGFSLG LP QE
Sbjct: 1373 TGSGEVVQNL TGRNLSDFLVKTYPRLVQGLKTKKWVNEVRYGGFSLG-GRDPGLPSGQE 1431

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
+ +++++ L + DR L +L + LD +++K+WFNKKGWH++ +F+N +
Sbjct: 1432 LGRSVEELWALLSPLPGGALDRVLKNTAWAHS LDAQDSLKIWFNNKGWHSMAFVNRAS 1491

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTQQLSEVALMTTSVD 284
NAILRA+L G + IT NHPLNLTQQLSE ALM +SVD
Sbjct: 1492 NAILRAHLPPGPARHAHSITTLNHPLNLTKEQLSEALMASSVD 1535

☐ >gi|15451838|ref|NP_150651.1| ☒ ATP-binding cassette, sub-family A, member 7, is
SS-N; macrophage ABC transporter [Homo sapiens]

gi|15042034|dbj|BAB62294.1| ☒ ABCA-SSN [Homo sapiens]
Length = 2008

Score = 243 bits (619), Expect = 3e-63

Identities = 125/284 (44%), Positives = 175/284 (61%), Gaps = 11/284 (3%)

Query: 1 FGKYPSELELQPMYNNENYTFVSNDAPEDTGTLELLNALT KDPGFGTRCMEGNPIPDTPCQ 60
FG YP+L L P MY +F S DAP D G LL AL ++ G + + P Q
Sbjct: 1125 FGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARLLEALLQEAG-----LEEPPVQ 1174

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
++ VP + + +GNWT ++PSPACQCS +++LP CP AGG PPPQ
Sbjct: 1175 HSSHRFSAPEVPAEVAKVLASGNWTPESPSPACQCSQPGARRLLPDCPAAAGGPPPPQAV 1234

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
+ +++Q+LTGRN+SD+LVKTY +++ + LK K WVNE RYGGFSLG LP QE
Sbjct: 1235 TGSGEVVQNL TGRNLSDFLVKTYPRLVQGLKTKKWVNEVRYGGFSLG-GRDPGLPSGQE 1293

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
+ +++++ L + DR L +L + LD +++K+WFNKKGWH++ +F+N +
Sbjct: 1294 LGRSVEELWALLSPLPGGALDRVLKNTAWAHS LDAQDSLKIWFNNKGWHSMAFVNRAS 1353

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTQQLSEVALMTTSVD 284
NAILRA+L G + IT NHPLNLTQQL E ALM +SVD
Sbjct: 1354 NAILRAHLPPGPARHAHSITTLNHPLNLTKEQLFEALMASSVD 1397

>gi|9506365|ref|NP_061985.1| ATP-binding cassette, sub-family A, member 7, iso
SS-N; macrophage ABC transporter [Homo sapiens]
gi|9211112|gb|AAF85794.1|AF250238.1 macrophage ABC transporter [Homo sapiens]
Length = 2146

Score = 242 bits (617), Expect = 5e-63
Identities = 125/284 (44%), Positives = 175/284 (61%), Gaps = 11/284 (3%)

Query: 1 FGKYP SLELQ P WMYNENYTFVSN DAPEDTGTLELLNALT KD PFGTRCMEGNPIPDT PCQ 60
FG YP+L L P MY +F S DAP D G LL AL ++ G + + P Q
Sbjct: 1263 FGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARLLEALLQEAG-----LEEPPVQ 1312

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKMLPVCPPGAGGLPPPQRK 120
++ VP + + +GNWT ++PSPACQCS +++LP CP AGG PPPQ
Sbjct: 1313 HSSHRSFAPEVPAEVAKVLASGNWTPESPSPACQCSQPGARRLLPDCPAAAGGPPPPQAV 1372

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
+ +++Q+LTGRN+SD+LVKTY +++ + LK K WVNE RYGGFSLG LP QE
Sbjct: 1373 TGSGEVVQNL TGRNLSDFLVKTYPRLV RQGLKTKK WVNE VRYGGFSLG-GRDPGLPSGQE 1431

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
+ +++++ L + DR L +L + LD ++++K+WFNNKGWH++ +F+N +
Sbjct: 1432 LGRSVEELWALLSPLPGGALDRVLKNLTAWAHSLDAQDSLKIWFNNKGWHSMVAFVNRAS 1491

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
NAILRA+L G + IT NHPLNLTK+QL E ALM +SVD
Sbjct: 1492 NAILRAHLPPGRARHAHSITTLNHPLNLTKQQLFEALMASSVD 1535

>gi|22725156|gb|AAN04657.1| ABC transporter ABCA7 [Homo sapiens]
Length = 2146

Score = 241 bits (615), Expect = 8e-63
Identities = 125/284 (44%), Positives = 175/284 (61%), Gaps = 11/284 (3%)

Query: 1 FGKYP SLELQ P WMYNENYTFVSN DAPEDTGTLELLNALT KD PFGTRCMEGNPIPDT PCQ 60
FG YP+L L P MY +F S DAP D G LL AL ++ G + + P Q
Sbjct: 1263 FGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARLLEALLQEAG-----LEEPPVQ 1312

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKMLPVCPPGAGGLPPPQRK 120
++ VP + + +GNWT ++PSPACQCS +++LP CP AGG PPPQ
Sbjct: 1313 HSSHRSFAPEVPAEVAKVLASGNWTPESPSPACQCSRPGARRLLPDCPAAAGGPPPPQAV 1372

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQE 180
+ +++Q+LTGRN+SD+LVKTY +++ + LK K WVNE RYGGFSLG LP QE
Sbjct: 1373 TGSGEVVQNL TGRNLSDFLVKTYPRLV RQGLKTKK WVNE VRYGGFSLG-GRDPGLPSGQE 1431

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
+ +++++ L + DR L +L + LD ++++K+WFNNKGWH++ +F+N +
Sbjct: 1432 LGRSVEELWALLSPLPGGALDRVLKNLTAWAHSLDAQDSLKIWFNNKGWHSMVAFVNRAS 1491

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
NAILRA+L G + IT NHPLNLTK+QL E ALM +SVD
Sbjct: 1492 NAILRAHLPPGPARHAHSITTLNHPLNLTKQQLFEALMASSVD 1535

>gi|15451840|ref|NP_038878.1| ATP-binding cassette, sub-family A, member 7 [M
gi|14209834|gb|AAK56862.1|AF287141.1 ATP-binding cassette transporter sub-famil
gi|14209836|gb|AAK56863.1| ATP-binding cassette transporter sub-family A member
Length = 2159

Score = 239 bits (610), Expect = 3e-62

Identities = 128/285 (44%), Positives = 176/285 (61%), Gaps = 2/285 (0%)

Query: 1 FGKYPSELELPWMYNENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
FG+YP L+L P MY +F S DAP D ++LL AL + G M+ + C
Sbjct: 1266 FGQYPPQLQLSPAMYGPQVSFFSEDAPGDPNRMKLLLEALLGEAGLQEPSMQDKDARGSECT 1325

Query: 61 AGEEEWTTAP-VPQTIMDLFQNGNWTMNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQR 119
+ T P VP + + +GNWT ++PSPACQCS +++LP CP GAGG PPPQ
Sbjct: 1326 HSLACYFTVPEVPPDVASILASGNWTPESPSPACQCSQPGARRLLPDCPAGAGGPPPPQA 1385

Query: 120 KQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQ 179
+++Q+LTGRN+SD+LVKTY ++ + LK K WV+E RYGGFSLG + LP
Sbjct: 1386 VAGLGEVVQNLGTGRNVSDFLVKTYPSLVRRGLKTKKWDEVRYGGFSLGGRDPD-LPTGH 1444

Query: 180 EVNDAIKQMKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
EV + +++ L ++ DR LN+L ++ GLD RN++K+WFNNKGWHA+ +F+N
Sbjct: 1445 EVVRTLAIEIRALLSPQPGNALDRILNLTQWALGLDARNSLKIWFNNKGWHAMVAFVNRA 1504

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
NN +L A L G + IT NHPLNLTK+QLSE L+ +SVD
Sbjct: 1505 NNGLLHALLPSGPVRHAHSITTLNHPLNLTKQQLSEATLIASSVD 1549

>gi|26342298|dbj|BAC34811.1| unnamed protein product [Mus musculus]
Length = 1487

Score = 228 bits (582), Expect = 7e-59

Identities = 97/107 (90%), Positives = 102/107 (95%)

Query: 1 FGKYPSELELPWMYNENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
FGKYPSELELPWMYNE YTFVSNDAPED GT ELLNALTKDPGFGTRCMEGNPIPDTPC
Sbjct: 1371 FGKYPSELELPWMYNEQYTFVSNDAPEDMGTQELLNALTKDPGFGTRCMEGNPIPDTPCL 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMNPSPACQCSSDKIKKMLPVC 107
AGEE+WT +PVPQ+I+DLFQNGNWTM+NPSPACQCSSDKIKKMLPVC
Sbjct: 1431 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVC 1477

>gi|20521748|dbj|BAA83014.2| KIAA1062 protein [Homo sapiens]
Length = 1771

Score = 99.8 bits (247), Expect = 4e-20

Identities = 72/219 (32%), Positives = 104/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMNPSPACQCSSDKIKKMLPVCPPGAGGLPP 116
P AG E WT+AP +P+ + + + C CS+ CP GG P
Sbjct: 952 PPTAGPEMWTSAPSLPRLVREPVR-----CTCSAQGTGFS---CPSSVGG-HP 995

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N
 Sbjct: 996 PQMRVVTGDILTDITGHNVSEYLLFT-----SDRFRL----HRYGAITFG--NVLKSI 1042

Query: 177 PSQEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 236
 P+ A ++K + R +V++NNKG+H++ ++L
 Sbjct: 1043 PASFGTRAPPMVRK-----IAVRRAAQVFYNNKGYHSMPTYL 1079

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
 N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 1080 NSLNNAILRANLPKSKGNPAAYGITVTNHPMNKTSASLS 1118

☐ >gi|11346269|pir|A59189 ATP-binding cassette transporter - human (fragment)
 Length = 1529

Score = 98.2 bits (243), Expect = 1e-19
 Identities = 72/219 (32%), Positives = 104/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMQNPSACQCSSDKIKKMLPVCPPGAGGLPP 116
 P AG E WT+AP +P+ + + + C CS+ CP GG P
 Sbjct: 710 PPTAGPEMWTSAAPSLPRLVREPVR-----CTCSAQGTGFS---CPSSVGG-HP 753

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N
 Sbjct: 754 PQMRVVTGDILTDITGHNVSEYLLFT-----SDRFRL----HRYGAITFG--NVLKSI 800

Query: 177 PSQEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 236
 P+ A ++K + R +V++NNKG+H++ ++L
 Sbjct: 801 PASFGTRAPPMVRK-----IAVRRAAQVFYNNKGYHSMPTYL 837

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
 N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 838 NSLNNAILRANLPKSKGNPAAYGITVTNHPMNKTSASLS 876

☐ >gi|14916523|sp|Q9BZC7|ABC2_HUMAN ATP-binding cassette, sub-family A, member 2 (transporter 2) (ATP-binding cassette 2)
 gi|13173236|gb|AAK14335.1| ☒ ABC transporter ABCA2 [Homo sapiens]
 Length = 2436

Score = 98.2 bits (243), Expect = 1e-19
 Identities = 72/219 (32%), Positives = 104/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMQNPSACQCSSDKIKKMLPVCPPGAGGLPP 116
 P AG E WT+AP +P+ + + + C CS+ CP GG P
 Sbjct: 1617 PPTAGPEMWTSAAPSLPRLVREPVR-----CTCSAQGTGFS---CPSSVGG-HP 1660

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N
 Sbjct: 1661 PQMRVVTGDILTDITGHNVSEYLLFT-----SDRFRL----HRYGAITFG--NVLKSI 1707

Query: 177 PSQEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 236
 P+ A ++K + R +V++NNKG+H++ ++L
 Sbjct: 1708 PASFGTRAPPMVRK-----IAVRRAAQVFYNNKGYHSMPTYL 1744

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274

N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 1745 NSLNNAILRANLPKSKGNPAAYGITVTNHPMNKTSASLS 1783

>gi|14550412|ref|NP_001597.1| ATP-binding cassette, sub-family A, member 2; K1
 sapiens]

gi|9957467|gb|AAG09372.1|AF178941_1 ATP-binding cassette sub-family A member 2
 gi|13173186|gb|AAK14334.1|AF327657_1 ABC transporter ABCA2 [Homo sapiens]
 Length = 2436

Score = 98.2 bits (243), Expect = 1e-19
 Identities = 72/219 (32%), Positives = 104/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMGNPSPACQCSSDKIKKMLPVCPPGAGGLPP 116
 P AG E WT+AP +P+ + + + C CS+ CP GG P
 Sbjct: 1617 PPTAGPEMWTSAAPSLPRLVREPVR-----CTCSAQGTGFS---CPSSVGG-HP 1660

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N
 Sbjct: 1661 PQMRVVTGDILTDITGHNVSLEYLLFT-----SDRFRL---HRYGAITFG--NVLKSI 1707

Query: 177 PSQEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 236
 P+ A ++K + R +V++NNKG+H++ ++L
 Sbjct: 1708 PASFGTRAPPMVRK-----IAVRRAAQVFYNNKGYHSMPTYL 1744

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
 N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 1745 NSLNNAILRANLPKSKGNPAAYGITVTNHPMNKTSASLS 1783

>gi|11993939|ref|NP_031405.1| ATP-binding cassette, sub-family A (ABC1), membe
 cassette 2 [Mus musculus]

gi|14916951|sp|P41234|ABC2_MOUSE ATP-binding cassette, sub-family A, member 2 (AT
 transporter 2) (ATP-binding cassette 2)

gi|11990231|emb|CAA53531.2| ABC transporter [Mus musculus]
 Length = 2434

Score = 97.4 bits (241), Expect = 2e-19
 Identities = 72/219 (32%), Positives = 103/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMGNPSPACQCSSDKIKKMLPVCPPGAGGLPP 116
 P AG E WT+AP +P+ + + + C CS+ CP GG P
 Sbjct: 1617 PPTAGPETWTSAPSLPRLVHEPVR-----CTCSAQGTGFS---CPSSVGG-HP 1660

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N Q
 Sbjct: 1661 PQMRVVTGDILTDITGHNVSLEYLLFT-----SDRFRL---HRYGAITFG--NVQKSI 1707

Query: 177 PSQEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 236
 P+ F + + + R +V +NNKG+H++ ++L
 Sbjct: 1708 PAS-----FGARVPPMVRKIAVRRVAQVLYNNKGYHSMPTYL 1744

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
 N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 1745 NSLNNAILRANLPKSKGNPAAYGITVTNHPMNKTSASLS 1783

>gi|14250599|gb|AAH08755.1|AAH08755 Similar to KIAA1062 protein [Homo sapiens]
Length = 867

Score = 96.7 bits (239), Expect = 3e-19

Identities = 71/219 (32%), Positives = 103/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTM QNPSACQCSSDKIKKMLPVCPPGAGGLPP 116
P AG E WT+AP +P+ + + + C CS+ CP GG P
Sbjct: 48 PPTAGPEMWT SAPSLPRLVREPVR-----CTCSAQGTGFS---CPSSVGG-HP 91

Query: 117 PQRKQNTADILQDLTGRNIDSYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALP 176
PQ + DIL D+TG N+S+YL+ T S + ++ RYG + G N
Sbjct: 92 PQMRVVAGDILTDITGHNVSEYLLFT-----SDRFRL---HRYGAITFG--NVLKSI 138

Query: 177 PSQEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 236
P+ A ++K + R +V++NNKG+H++ ++L
Sbjct: 139 PASFGTRAPPMVRK-----IAVRRAAQVFYNNKGYHSMPTYL 175

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
N +NNAILRANL K + NP+ YGIT NHP+N T LS
Sbjct: 176 NSLNNAILRANLPKSKGNPAAYGITVTNHPMNKTSASLS 214

>gi|1082239|pir||B54774 ATP binding cassette transporter ABC2 - mouse (fragment)
Length = 1472

Score = 95.5 bits (236), Expect = 7e-19

Identities = 71/219 (32%), Positives = 102/219 (46%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTM QNPSACQCSSDKIKKMLPVCPPGAGGLPP 116
P AG E WT+AP +P+ + + + C CS+ CP GG P
Sbjct: 654 PPTAGPETWTSAPSLPRLVHEPVR-----CTCSAQGTGFS---CPSSVGG-HP 697

Query: 117 PQRKQNTADILQDLTGRNIDSYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALP 176
PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N Q
Sbjct: 698 PQMRVVTGDILTDTITGHNVSEYLLFT-----SDRFRL---HRYGAITFG--NVQKSI 744

Query: 177 PSQEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 236
P+ F + + R +V +NNKG+H++ ++L
Sbjct: 745 PAS-----FGARVPPMVRKIAVRRVAQVLYNNKGYHSMPTYL 781

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
N +NNAILRANL K + NP+ Y IT NHP+N T LS
Sbjct: 782 NSLNNAILRANLPKSKGNPAAIXITVTNHPMNKTSASLS 820

>gi|13242308|ref|NP_077372.1| ATP-binding cassette, sub-family A (ABC1), member
norvegicus]

gi|10799949|dbj|BAB16596.1| ABC2 [Rattus norvegicus]
Length = 2434

Score = 94.7 bits (234), Expect = 1e-18

Identities = 72/219 (32%), Positives = 102/219 (46%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTM QNPSACQCSSDKIKKMLPVCPPGAGGLPP 116

P AG E WT AP +P+ + + + C CS+ CP GG P
 Sbjct: 1617 PPTAGPETWTWAPSLPRLVHEPVR-----CTCSAQGTGFS---CPSSVGG-HP 1660

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N Q
 Sbjct: 1661 PQMRVVTGDILTDITGHNVSLEYLLFT-----SDRFRL---HRYGAITFG--NIQKSI 1707

Query: 177 PSQEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 236
 P+ ++K + R +V +NNKG+H++ ++L
 Sbjct: 1708 PAPIGTRTPLMVRK-----IAVRRVAQVLYNNKGYHSMPTYL 1744

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
 N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 1745 NSLNNAILRANLPKSKGNPAAYGITVTNHPMNKTSASLS 1783

>gi|27881503|ref|NP_775099.1| ATP-binding cassette, sub-family A, member 12 is
 cassette A12 [Homo sapiens]
 Length = 2347

Score = 81.6 bits (200), Expect = 1e-14
 Identities = 72/286 (25%), Positives = 123/286 (43%), Gaps = 78/286 (27%)

Query: 4 YPSLELQPMY--NENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPC-- 59
 YP +++ P +Y +E F +N P T L++A+ PG C+ + D C
 Sbjct: 1526 YPEIQISPSLYGTSEQTAFYANYHPS---TEALVSAMWDFPGIDNMCLNTS---DLQCLN 1579

Query: 60 QAGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSSDKIKKMLPVCPPGAGGLPPPQR 119
 + E+W T+ P T + C CS + + CP PP R
 Sbjct: 1580 KDSLEKWNTSGEPITNFGV-----CSCSEN-----VQCEP--KFNYSPPHR 1618

Query: 120 KQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSQ 179
 + ++ ++ +LTG+ + +YL+ T + + K RYGG+S G
 Sbjct: 1619 RTYSSQVIYNLTGQRVENYLISTANEFVQK-----RYGWSFG----- 1656

Query: 180 EVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLD-TRNNVKVWFNNKGWHAISSFLNV 238
 L L KD D +TG+ R KVV++ +G+H++ ++LN
 Sbjct: 1657 -----LPLTKDLRFD-----ITGVPANRTLAKVWYDPEGYHSLPAYLNS 1695

Query: 239 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NN +LR N+ K + H GI ++HP + Q E A +++ +D
 Sbjct: 1696 LNNFLLRVNMSKYDAARH-GIIMYSHYPYGVQDQ--EQATISSLID 1738

>gi|27881501|ref|NP_056472.2| ATP-binding cassette, sub-family A, member 12 is
 cassette A12 [Homo sapiens]
 Length = 2277

Score = 81.6 bits (200), Expect = 1e-14
 Identities = 72/286 (25%), Positives = 123/286 (43%), Gaps = 78/286 (27%)

Query: 4 YPSLELQPMY--NENYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPC-- 59
 YP +++ P +Y +E F +N P T L++A+ PG C+ + D C
 Sbjct: 1456 YPEIQISPSLYGTSEQTAFYANYHPS---TEALVSAMWDFPGIDNMCLNTS---DLQCLN 1509

Query: 60 QAGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSSDKIKKMLPVCPPGAGGLPPPQR 119
 + E+W T+ P T + C CS + + CP PP R

Sbjct: 1510 KDSLEKWNTSGEPITNFGV-----CSCSEN-----VQECF--KFNYSPPHR 1548

Query: 120 KQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQ 179
 + ++ ++ +LTG+ + +YL+ T + + K RYGG+S G

Sbjct: 1549 RTYSSQVIYNLTGQRVENYLISTANEFVQK-----RYGGWSFG----- 1586

Query: 180 EVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLD-TRNNVKVWFNNKGWHAISSFLNV 238
 L L KD D +TG+ R KVV++ +G+H++ ++LN

Sbjct: 1587 -----LPLTKDLRFD-----ITGVPANRTLAKVWYDPEGYHSLPAYLNS 1625

Query: 239 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NN +LR N+ K + H GI ++HP + Q E A +++ +D

Sbjct: 1626 LNNFLLRVNMSKYDAARH-GIIMYSHPYPGVQDQ--EQATISSLID 1668

>gi|23957299|gb|AAN40735.1|AF418105_1 ATP-binding cassette transporter family
 Length = 2347

Score = 81.6 bits (200), Expect = 1e-14
 Identities = 72/286 (25%), Positives = 123/286 (43%), Gaps = 78/286 (27%)

Query: 4 YPSLELQPWMY--NENYTFVSNDAPEDTGTLELLNALT KD PGFGTRCMEGNPIPDTPC-- 59
 YP +++ P +Y +E F +N P T L++A+ PG C+ + D C

Sbjct: 1526 YPEIQISPSLYGTSEQTAFYANYHPS---TEALVSAMWDFPGIDNMCLNTS---DLQCLN 1579

Query: 60 QAGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQR 119
 + E+W T+ P T + C CS + + CP PP R

Sbjct: 1580 KDSLEKWNTSGEPITNFGV-----CSCSEN-----VQECF--KFNYSPPHR 1618

Query: 120 KQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQ 179
 + ++ ++ +LTG+ + +YL+ T + + K RYGG+S G

Sbjct: 1619 RTYSSQVIYNLTGQRVENYLISTANEFVQK-----RYGGWSFG----- 1656

Query: 180 EVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLD-TRNNVKVWFNNKGWHAISSFLNV 238
 L L KD D +TG+ R KVV++ +G+H++ ++LN

Sbjct: 1657 -----LPLTKDLRFD-----ITGVPANRTLAKVWYDPEGYHSLPAYLNS 1695

Query: 239 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NN +LR N+ K + H GI ++HP + Q E A +++ +D

Sbjct: 1696 LNNFLLRVNMSKYDAARH-GIIMYSHPYPGVQDQ--EQATISSLID 1738

>gi|14189735|gb|AAK54355.1| ATP-binding cassette transporter family A member 1
 Length = 2277

Score = 81.6 bits (200), Expect = 1e-14
 Identities = 72/286 (25%), Positives = 123/286 (43%), Gaps = 78/286 (27%)

Query: 4 YPSLELQPWMY--NENYTFVSNDAPEDTGTLELLNALT KD PGFGTRCMEGNPIPDTPC-- 59
 YP +++ P +Y +E F +N P T L++A+ PG C+ + D C

Sbjct: 1456 YPEIQISPSLYGTSEQTAFYANYHPS---TEALVSAMWDFPGIDNMCLNTS---DLQCLN 1509

Query: 60 QAGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQR 119
 + E+W T+ P T + C CS + + CP PP R

Sbjct: 1510 KDSLEKWNTSGEPITNFGV-----CSCSEN-----VQECF--KFNYSPPHR 1548

Query: 120 KQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQ 179

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      +  ++ ++ +LTG+ + +YL+ T  + + K          RYGG+S G
Sbjct: 1549 RTYSSQVIYNLTGQRVENYLISTANEFVQK-----RYGGWSFG----- 1586

Query: 180 EVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLD-TRNNVKVWFNNKGWHAISSFLNV 238
          L L KD  D          +TG+  R  KVW++ +G+H++ ++LN
Sbjct: 1587 -----LPLTKDLRFD-----ITGVPANRTLAKVWYDPEGYHSLPAYLNS 1625

Query: 239 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
      +NN +LR N+ K +  H GI  ++HP  + Q  E A +++ +D
Sbjct: 1626 LNNFLLRVNMSKYDAARH-GIIMYSHPYPGVQDQ--EQATISSLID 1668

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[gi|27684549|ref|XP_237242.1|](#) similar to ATP-binding cassette transporter fami
sapiens] [Rattus norvegicus]
Length = 1699

Score = 74.7 bits (182), Expect = 1e-12
Identities = 70/285 (24%), Positives = 122/285 (42%), Gaps = 76/285 (26%)

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Query: 4  YPSLELQPWMY--NENYTFVSNDAPEDTGTLELLNALT KD PGFGTRCMEGNPIPDTPCQA 61
      YP L + P +Y +E  F +N P  T  L++AL  PG  C+  +  D+ C
Sbjct: 878 YPELLISPSIYGNSEQTAFYANFDPS---TNALVSALWNFP GIDNVCLNTS---DSQCLK 931

Query: 62  GEE--EWT TAPVPQTIMDLFQNGNWTM QNPS PACQCSSDKIKKMLPVCPPGAGGLPPPQR 119
      +  +W T+  +D F  C C SD +++  CP  PP R
Sbjct: 932 KDNLGKWNTS---GEAIDNFG-----VCSC-SDNVQE---CP--KFNYSPPHR 970

Query: 120 KQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQ 179
      +  ++ ++ +LTG+++ +YL+ T  + K          RYGG+S G
Sbjct: 971 RTYSSQVIYNLTGKHMENYLISTANHFVQK-----RYGGWSFG----- 1008

Query: 180 EVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
          +KL D  D  + R +          KVW++ +G+H++ ++LN +
Sbjct: 1009 -----MKLTNDLRFDVTA VPVNRTLA-----KVWYDPEGYHSLPAYLNSL 1048

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
      NN +LR N+ + +  H GI  ++HP  + Q  E A +++ +D
Sbjct: 1049 NNFLLRVNMSEYDAARH-GIIMYSHPYPGVQDQ--EQATISSLID 1090

```

[gi|25141343|ref|NP_490949.2|](#) ABC transporter family member [Caenorhabditis eleg
[gi|20198808|gb|AAK21369.2|](#) Hypothetical protein F12B6.1 [Caenorhabditis elegans]
Length = 1547

Score = 71.6 bits (174), Expect = 1e-11
Identities = 59/188 (31%), Positives = 86/188 (45%), Gaps = 40/188 (21%)

```

Query: 122 NTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEV 181
      NT D + DLTGRN++ + + T  +A +          F GGFSLG  N +A  SQ
Sbjct: 743 NTTDRIFDLTGRNLTQFRLITRFAQLANT-----TAPFFLGGFSLGHVNQRA--QSQAD 794

Query: 182 ND-----AIKQMKKHLKL-----AKDSSADRFLNSLGRFMTGL 214
      D          IK + + +++          A++ + ++ +N L  +  L
Sbjct: 795 IDTSKRGWLETIKDIAQSMRIINLNTTGIEPATPKVLDPPFAQNITLNQVVNDL---LQNL 851


Query: 215 DTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQKGENPSHYGITAFNHPLNLT-KQQL 273
      D R  NVKVWFNNK W          N+++NA+LR          +P  GI  NHP+N T  Q  L

```

Sbjct: 852 DVRENVKVVWFNNKIWPGFPIASNILSNALLRQE-DYAIDPEDLGILTMNHPMNKTISQTL 910

Query: 274 SEVALMTT 281
+ AL T

Sbjct: 911 DQNALKFT 918

 >gi|7498949|pir||T15200 hypothetical protein F12B6.1 - Caenorhabditis elegans
Length = 1447

Score = 70.9 bits (172), Expect = 2e-11

Identities = 59/188 (31%), Positives = 86/188 (45%), Gaps = 40/188 (21%)

Query: 122 NTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEV 181

NT D + DLTGRN++ + + T +A + F GGFSLG N +A SQ

Sbjct: 743 NTTDRIFDLTGRNLTQFRLITRFAQLANT-----TAPFFLGGFSLGHVNQRA--QSQAD 794

Query: 182 ND-----AIKQMKKHLKL-----AKDSSADRFLNSLGRFMTGL 214
D IK + + +++ A++ + ++ +N L + L

Sbjct: 795 IDTSKRGWLETIKDIAQSMRIINLNTTGIEPATPKVLDPPFAQNITLNQVVNDL---LQNL 851


Query: 215 DTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQKGENPSHYGITAFNHPLNLT-KQQ 273

D R NVKVVWFNNK W N+++NA+LR +P GI NHP+N T Q L

Sbjct: 852 DVRENVKVVWFNNKIWPGFPIASNILSNALLRQE-DYAIDPEDLGILTMNHPMNKTISQTL 910

Query: 274 SEVALMTT 281
+ AL T

Sbjct: 911 DQNALKFT 918

 >gi|21297828|gb|EAA09973.1| agCP11808 [Anopheles gambiae str. PEST]
Length = 1725

Score = 58.5 bits (140), Expect = 1e-07

Identities = 25/63 (39%), Positives = 41/63 (65%), Gaps = 4/63 (6%)

Query: 222 VWFNNKGWHAISSFLNVINNAILRANLQKGENPSHYGITAFNHPLNLTQQLSEVALMTT 281



VW+NNKG+H++ ++LN+++ A+LRA L N S Y I NHPL + + +LS +++

Sbjct: 1051 VWYNNKGYHSMPTWLNMLDTAVLRAEL----NDSSYTIRTINHPLKIEEDELVSMSLQQ 1106

Query: 282 SVD 284

D

Sbjct: 1107 IAD 1109

 >gi|20850354|ref|XP_136692.1|  similar to ATP-binding cassette transporter fami
sapiens] [Mus musculus]
Length = 1670

Score = 58.2 bits (139), Expect = 1e-07

Identities = 42/165 (25%), Positives = 74/165 (44%), Gaps = 51/165 (30%)

Query: 93 CQCSSDKIKKMLPVCPPGAGGLPPPQKQNTADILQDLTGRNISDYLVKTYVQIIAKSLK 152

C C SD +++ CP PP R+ ++ ++ +LTG+++ +YL+ T + K

Sbjct: 1533 CSC-SDNVQE----CP--KFNYHPPHRRTYSSQVIYNLTGKHMENYLITTANHFVQK--- 1582

Query: 153 NKIWVNEFRYGGFSLGVSNTQALPPSQEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMT 212
 RYGG+S G +KL D D +T
 Sbjct: 1583 -----RYGWSFG-----MKLTNDLRFD-----VT 1602

Query: 213 GL-DTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQKGENPSH 256
 + D R KVV++ +G+H++ ++LN +NN +LR N+ + + H
 Sbjct: 1603 AVPDNRTLAKVWYDPEGYHSLPAYLNSLNNFLLRVNMSEYDAARH 1647

>gi|24643648|ref|NP_608437.1| CG1819-PA [Drosophila melanogaster]
 gi|22832643|gb|AAF50847.2| CG1819-PA [Drosophila melanogaster]
 Length = 1591

Score = 47.0 bits (110), Expect = 3e-04
 Identities = 29/92 (31%), Positives = 47/92 (51%), Gaps = 11/92 (11%)

Query: 199 SADRFLNSLGRFMT-----GLDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQKGE 252
 S D LNS G + GL+ + VW+NNKG+H++ ++LN +N+ +LR +
 Sbjct: 892 SYDWVLNSWGEYSERRYGGYGLNG-SGATVWYNNKGYHSMMAWLNDLNSELLRTM---- 946

Query: 253 NPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 N S I N P L +LS +++ + D
 Sbjct: 947 NDESSILTLNEPWKLGFELSTSSILRQAGD 978

>gi|27697650|ref|XP_223630.1| similar to hypothetical protein FLJ33951 [Homo s
 norvegicus]
 Length = 1132

Score = 38.5 bits (88), Expect = 0.11
 Identities = 15/27 (55%), Positives = 21/27 (77%)

Query: 222 VWFNNKGWHAISSFLNVINNAILRANL 248
 VW+N KG+H++ S+LN +NN IL NL
 Sbjct: 178 VWYNQKGFHSLPSYLNHLNLLILWQNL 204

>gi|15610478|ref|NP_217859.1| hypothetical protein Rv3342 [Mycobacterium tubercu
 gi|6137297|sp|O53392|YX42_MYCTU Putative methyltransferase RV3342
 gi|7477581|pir|E70846 hypothetical protein Rv3342 - Mycobacterium tuberculosis
 H37RV)
 gi|2894252|emb|CAA17114.1| hypothetical protein Rv3342 [Mycobacterium tuberculosi
 Length = 243

Score = 34.3 bits (77), Expect = 2.3
 Identities = 22/88 (25%), Positives = 39/88 (44%)

Query: 21 VSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIDTPCQAGEEEWTTAPVPQTIMDLFQ 80
 V N E G + L + G R P P T Q + EWT PQ ++DL
 Sbjct: 134 VWNTRDERLGVVRELGEIIGRDGDPVRDRVTLPEPFTTVQRHQVEWTNYLTPQALIDLVA 193

Query: 81 NGNWTMQNPSPACQCSSDKIKKMLPVCP 108
 + ++ + +P+ + D+++++L P
 Sbjct: 194 SRSYCITSPAQVRTKTLDRVRQLLATHP 221

☐ >gi|15842938|ref|NP_337975.1| methyltransferase, putative [Mycobacterium tubercu
gi|13883273|gb|AAK47789.1| methyltransferase, putative [Mycobacterium tuberculosi
Length = 236

Score = 33.9 bits (76), Expect = 2.4
Identities = 22/88 (25%), Positives = 39/88 (44%)

Query: 21 VSNDAPEDTGTLELLNALT KDPGFTRCMEGNPIPDTPCQAGEEEWTTAPVPQTIMDLFQ 80
V N E G + L + G R P P T Q + EWT PQ ++DL
Sbjct: 127 VWNTRDERLGWVRELGEIIGRDGDPVRDRVTLPEPFTTVQRHQVEWTNYLTPQALIDLVA 186

Query: 81 NGNWTMQNPSPACQCSSDKIKKMLPVCP 108
+ + + + +P+ + D+++++L P
Sbjct: 187 SRSYCITSPAQVVRTKTLDRVRQLLATHP 214

☐ >gi|20088939|ref|NP_615014.1| conserved hypothetical protein [Methanosarcina ace
C2A]
gi|19913785|gb|AAM03494.1| conserved hypothetical protein [Methanosarcina acetivo
C2A]
Length = 345

Score = 33.9 bits (76), Expect = 2.6
Identities = 31/114 (27%), Positives = 54/114 (47%), Gaps = 13/114 (11%)

Query: 100 IKKMLPVCPPGAGGLPPPQKQNTADILQDLTGRN-ISDYLV-----KTYVQIIAKS 150
+K L VC P + L R + DI++D R I LV K Y ++I ++
Sbjct: 214 LKTYLRVCQPKSPAL--WDRINESLDIMKDKCSRTVIRTTLVKGENIFNPKGYAELIKRA 271

Query: 151 LKNKIWVNEFRYGGFSLGVSNTQALPPSQEVNDAIKQMKKHL--KLAKDSSADR 202
+ + + + + GFS + A+P +EV + K++ KHL ++A +S R
Sbjct: 272 SPDFVEIKAYMHLGFSRLRLDRSAMPTHEEVLEFSKELAKHLGYEIADESEISR 325

☐ >gi|1172578|sp|Q08304|PPOB_LYCES Polyphenol oxidase B, chloroplast precursor (PI
oxidase)
gi|1076593|pir||S33540 catechol oxidase (EC 1.10.3.1) B precursor [similarity] -
gi|22727|emb|CAA78296.1| polyphenol oxidase precursor [Lycopersicon esculentum]
Length = 596

Score = 33.9 bits (76), Expect = 2.8
Identities = 30/93 (32%), Positives = 44/93 (47%), Gaps = 6/93 (6%)

Query: 166 SLGVSNTQALPPSQEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFN 225
S+G NT LPP+ EV + +M K + A + A + T NN++ ++
Sbjct: 445 SVGKVNTSTLPPANEVF-PLAKMDKTISFAINRPASSRTQQEKNEQEEMLTFFNNIR--YD 501

Query: 226 NKGWHAISSFLNVINNAILRAN-LQKGENPSHY 257
N+G+ FLNV NN + AN L K E Y
Sbjct: 502 NRGYIRFDVFLNVDNN--VNANELDKAEFAGSY 532

☐ >gi|20899064|ref|XP_139895.1| ☒ similar to ATP-binding cassette, sub-family A me
cassette 3; ABC transporter 3 [Homo sapiens] [Mus
musculus]


Length = 1686

Score = 33.5 bits (75), Expect = 3.2

Identities = 21/65 (32%), Positives = 34/65 (52%), Gaps = 5/65 (7%)

Query: 214 LDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQGENPSHYGITAFNHPLNLTKQQL 273
 ++ VK FNN+ +H+ S L +++N + + L G N S IT N+P T ++
 Sbjct: 967 VNNHTTVKALFNNQAYHSPSLALTLVDNLLFK--LLSGANAS---ITTTNYPQPQTAIEV 1021

Query: 274 SEVAL 278
 SE L
 Sbjct: 1022 SESIL 1026

 >gi|21227448|ref|NP_633370.1| Fe-S oxidoreductase [Methanosarcina mazei Goel]
 gi|20905817|gb|AAM31042.1| Fe-S oxidoreductase [Methanosarcina mazei Goel]
 Length = 365

Score = 33.1 bits (74), Expect = 4.3

Identities = 30/114 (26%), Positives = 54/114 (47%), Gaps = 13/114 (11%)

Query: 100 IKKMLPVCPPGAGGLPPPQRKQNTADILQDLTGRN-ISDYLVK-----TYVQIIAKS 150
 ++ L +C P + L R + DI++D + R I LVK Y ++I K+
 Sbjct: 238 LETYLRICQPKSPAL--WDRINESLDIMKDKSSRTVIRTTLVKGENIFNPEGYAEMIKKA 295

Query: 151 LKNKIWNNEFRYGGFSLGVSNTQALPPSQEVNDAIKQMKKHL--KLAKDSSADR 202
 + + + + + GFS A+P +EV + K++ KHL ++A +S R
 Sbjct: 296 SPDFVEIKAYMHLGFSRLRLERSAMPSHEEVLEFSKELAKHLGYEIADESEISR 349

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF

Posted date: Feb 3, 2003 1:28 AM

Number of letters in database: 424,737,763

Number of sequences in database: 1,326,269

Lambda	K	H
0.315	0.133	0.407

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 263,239,907

Number of Sequences: 1326269

Number of extensions: 12084886

Number of successful extensions: 31048

Number of sequences better than 10.0: 58

Number of HSP's better than 10.0 without gapping: 46

Number of HSP's successfully gapped in prelim test: 12
Number of HSP's that attempted gapping in prelim test: 30923
Number of HSP's gapped (non-prelim): 75
length of query: 284
length of database: 424,737,763
effective HSP length: 122
effective length of query: 162
effective length of database: 262,932,945
effective search space: 42595137090
effective search space used: 42595137090
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.6 bits)
S2: 72 (32.3 bits)